PATENT APPLICATION

METHODS OF PROGNOSIS OF PROSTATE CANCER

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METHODS OF PROGNOSIS OF PROSTATE CANCER

This application claims the benefit of provisional application, 60/391,309, filed June 24, 2002, which is incorporated herein in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are outcome prognostic in prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer will account for an estimated 30% (189,000) of new cancer cases in men in the United States in 2002 (1). Many of these newly diagnosed cases are a result of the extensive use of prostate-specific antigen (PSA) screening and the subsequent diagnosis of prostate cancer at an early stage and age. However, despite the introduction of PSA screening the mortality from prostate cancer has remained relatively constant. The implications of this are that: (1) there are a large group of men diagnosed with prostate cancer for whom radical treatment is probably unnecessary and who will die with their prostate cancer rather than from it; and (2) there are a group of men for whom early detection offers the possibility of cure that may be denied by delay. Consequently, identifying these groups of men at the time of diagnosis is critical to the optimal management of prostate cancer.

While the benefits of PSA screening are widely debated, this serum marker remains one of only a small number of preoperative parameters of prognostic utility. In order to enhance the predictive value of individual parameters with outcomes, nomograms have been developed that incorporate parameters that are measured routinely in clinical practice to predict the probability of PSA relapse free survival of individual patients both prior to and following therapy (2-6). Models such as these currently form the basis of routine clinical decision-making, but such classification systems cannot explore differences in outcomes observed between cancers with similar histopathological features. Hence, there remains a critical need for increased accuracy in the subcategorization of prostate cancers to identify those with an aggressive phenotype.

There are a considerable number of publications assessing the ability of biomarkers to predict an earlier time to relapse of prostate cancer following radical prostatectomy (reviewed in ref. (17)). Despite these data, there remain no molecular markers of routine clinical utility which differentiate localized prostate cancers with an aggressive phenotype, and clinicians still rely on conventional preoperative and postoperative prognostic indicators such as pretreatment PSA levels, pathological stage and Gleason grade in routine decision-making. This most likely reflects the fact that studies that have correlated differences in gene expression with patient outcome have assessed candidate genes with limited predictive power that provide no additional prognostic information above the conventional variables. This accentuates the need to discover novel genes with strong predictive ability.

One approach is to define patterns of gene expression that correlate with disease phenotype and patient outcome. Here, we undertook a systematic search for novel biomarkers of prostate cancer prognosis by outcome-based analyses of transcript profiles.

SUMMARY OF INVENTION

The present invention evaluates gene expression profile and identifies prognostic genes of prostate cancers. The present invention provides a method of determining prognosis of prostate cancer and predicting prostate cancer outcome of a patient. The method comprises the steps of first establishing the threshold value of at least one prognostic gene of prostate cancer. Then, the amount of the prognostic gene from a prostate tissue of a patient inflicted of prostate cancer is determined. The amount of the prognostic gene present in that patient is compared with the established threshold value of the prognostic gene, whereby the prognostic outcome of the patient is determined.

In certain embodiments, the amount of the prognostic gene is determined by the quantitation of a transcript encoding the sequence of the prognostic gene; or a polypeptide encoded by the transcript. The quantitation of the transcript can be based on hybridization to the transcript. The quantitation of the polypeptide can be based on antibody detection. The method optionally comprises a step of amplifying nucleic acids from the tissue sample before the evaluating. In some embodiments, the evaluating is of a plurality of sequences. The method may further comprises determining prostate-specific antigen (PSA) level. The prognosis contributes to selection of a therapeutic strategy.

BRIEF DESCRIPTION OF THE FIGURES

The file of this patent contains at least one drawing executed in color. Copies of this patent with color drawing(s) will be provided by the Patent and Trademark Office upon request and payment of the necessary fee.

Figure 1 shows cluster analysis of prostate cancer samples from 72 patients treated for localised prostate cancer by RP. Each column represents a single RP specimen and each row represents one of the 264 genes which demonstrated a strong association with PSA relapse in our model. The dendogram at the top shows the degree to which each prostate cancer is related to the others with respect to gene expression. The 17 patients known to have experienced a PSA relapse are indicated by an "R". The relative level of expression is indicated by the color scale at the bottom and is indicative of the normalized average intensity units of fluorescence signal detected by microarray analysis.

Figure 2A shows the expression of *trp-p8* mRNA detected by oligonucleotide microarray in prostate cancer samples and in normal body tissues. Samples are: prostate cancer 1-74, adrenal glands 75-77, aorta 78-80, artery 81-83, bladder 84-86, bone marrow 87-89, colonic epithelium 90-92, cerebral cortex 93-95, colon 96-98, colonic muscle 99-101, esophagus 102-104, heart 105-107, kidney 108-110, liver 111-113, lung 114-116, lymph node 117-119, muscle 120-122, oral mucosa 123-125, pharyngeal mucosa 126-128, pancreas 129-131, parathyroid glands 132-133, pituitary 134-136, prostate 137-143, retina 144-146, skin 147-149, small intestine 150-152, spleen 153-155, stomach 156-158, trachea 159-161, tongue 162-164, ureter 165-167, vagus nerve 168-170, vein 171-174.

Figure 2B shows the expression of *trp-p8* mRNA, and **Figure 2C** shows the PSA mRNA; both detected by oligonucleotide microarray in LuCaP-35 tumors at days 0 to 100 post castration. The expression level of *trp-p8* and PSA is shown as normalized average intensity units (Y-axis) of fluorescence signal detected by microarray analysis.
units (Y-axis) of fluorescence signal detected by microarray analysis.

Figure 3 shows the *Trp-p8* mRNA expression detected by *in situ* hybridization in radical prostatectomy cases treated with or without neoadjuvant hormone therapy prior to surgery. **Figure 3A**: A prostate cancer from a patient treated with RP only showing positive *trp-p8* mRNA expression in malignant prostate epithelium. **Figure 3B:** A prostate cancer from a patient treated with RP and NHT showing positive *trp-p8* mRNA expression. **Figure 3C:** A prostate cancer from a patient treated with RP only with no detectable *trp-p8* mRNA expression in the malignant epithelium, and **Figure D:** A prostate cancer from a patient treated with preoperative NHT with no evidence of *trp-p8* expression.

Figure 4A shows the *trp-p8* protein sequence. **Figure 4B** shows the *trp-p8* mRNA sequence.

DETAILED DESCRIPTION OF INVENTION

Current models of prostate cancer classification are poor at distinguishing between tumors that have similar histopathological features but vary in clinical course and outcome. In the present invention, we have applied classical survival analysis to genome-wide gene expression profiles of prostate cancers and preoperative prostate-specific antigen levels from each patient, to identify prognostic markers of disease relapse that provide additional predictive value relative to prostate-specific antigen concentration. The present invention demonstrates that multivariable survival analysis can be applied to gene expression profiles of prostate cancers with censored follow-up data and used to identify molecular markers of prostate cancer relapse with strong predictive power and relevance to the etiology of this disease.

Prostate Cancer and Treatments

Prostate cancer is found mainly in older men. Prostate cancer is the most commonly diagnosed internal malignancy and second most common cause of cancer death in men in the U.S., resulting in approximately 40,000 deaths each year. Landis et al. (1998) CA Cancer J. Clin. 48:6-29; and Greenlee, et al. (2000) CA Cancer J. Clin. 50:7-13. The incidence of prostate cancer has been increasing rapidly over the past 20 years in many parts of the world. Nakata, et al. (2000) Int. J. Urol. 7:254-257; and Majeed, et al. (2000) BJU Int. 85:1058-1062. It develops as the result of a pathologic transformation of normal prostate cells. In tumorigenesis, the cancer cell undergoes initiation, proliferation, and loss of contact inhibition, culminating in invasion of surrounding tissue and, ultimately, metastasis.

Prostate cancer is a disease in which malignant (cancer) cells form in the tissues of the prostate. The prostate is a gland in the male reproductive system located just below the bladder (the organ that collects and empties urine) and in front of the rectum (the lower part of the intestine). It is about the size of a walnut and surrounds part of the urethra (the tube that empties urine from the bladder). The prostate gland produces fluid that makes up part of the semen. See generally, Boyle, et al. (2002) Textbook of Prostate Cancer Isis Medical Media, ISBN: 1901865304; Kantoff (ed. 2002) Prostate Cancer: Principles and Practice Lippincott, ISBN: 0781720060; Carroll (2001) Prostate Cancer Decker, ISBN: 1550091301; Belldegrun, et al. (2000) New Perspectives in Prostate Cancer Isis Medical Media, ISBN: 1901865568; Lepor (1999) Prostatic Diseases Saunders, ISBN: 072167416X; Petrovich, et al. (eds. 1996) Carcinoma of the Prostate: Innovations in Management, Springer Verlag, ISBN: 3540587497; and standard prostate cancer medical texts.

Four types of standard treatment are used for prostate cancer: watchful waiting, surgery, radiation therapy, or hormone ablation therapy. See, e.g., the National Cancer Institute (NCI) description of prostate cancer, www.cancer.gov.

Watchful waiting is closely monitoring a patient's condition but withholding treatment until symptoms appear or change. This is usually used in older men with other medical problems and early stage disease.

Surgery is usually offered to prostate cancer patients in good health who are younger than 70 years old. Main surgery options are pelvic lymphadenectomy, radical protatectomy, perineal prostatectomy, and transurethral resection of the prostate.

Pelvic lymphadenectomy is a surgical procedure to take out lymph nodes in the pelvis to see if they contain cancer. If the lymph nodes contain cancer, the doctor will not remove the prostate and may recommend other treatment. Radical prostatectomy (RP) is surgery to remove the entire prostate. Radical prostatectomy is done only if tests show the cancer has not spread outside the prostate. The two types of radical prostatectomy are retropubic prostatectomy, which removes the prostate through an incision made in the abdominal wall, and removal of surrounding lymph nodes (lymphadenectomy) can be done at the same time; and perineal prostatectomy, which is surgery to remove the prostate through an incision made between the scrotum and the anus, and if surrounding lymph nodes are to be removed, this is usually done through a separate incision. Transurethral resection of the prostate is a surgical procedure to remove tissue from the prostate using an instrument inserted through the urethra. This operation

is sometimes done to relieve symptoms caused by the tumor before other treatment is given. Transurethral resection of the prostate may also be done in men who cannot have a radical prostatectomy because of age or illness.

Impotence and leakage of urine from the bladder or stool from the rectum may occur in men treated with surgery. In some cases, doctors can use a technique known as nerve-sparing surgery. This type of surgery may save the nerves that control erection. However, men with large tumors or tumors that are very close to the nerves may not be able to have this surgery.

Radiation therapy is the use of x-rays or other types of radiation to kill cancer cells and shrink tumors. Radiation therapy may use external radiation (using a machine outside the body) or internal radiation. Internal radiation involves putting radioisotopes (materials that produce radiation) through thin plastic tubes into the area where cancer cells are found. Prostate cancer is treated with external and internal (implant) radiation. Radiation therapy may be used alone or in addition to surgery. Impotence and urinary problems may occur in men treated with radiation therapy.

Hormone therapy is the fourth of the standard treatments. Hormones are chemicals produced by glands in the body and circulated in the bloodstream. Hormone therapy is the use of hormones to stop cancer cells from growing. Male hormones (especially testosterone) can help prostate cancer grow. To stop the cancer from growing, female hormones or drugs that decrease production of male hormones may be given. Hormone therapy used in the treatment of prostate cancer may include the following: estrogens (hormones that promote female sex characteristics) can prevent the testicles from producing testosterone, however, estrogens are seldom used today in the treatment of prostate cancer because of the risk of serious side effects; luteinizing hormone-releasing hormone agonists also can prevent the testicles from producing testosterone, e.g., leuprolide, goserelin, and buserelin; antiandrogens can block the action of androgens (hormones that promote male sex characteristics), two examples are flutamide and bicalutamide; drugs that can prevent the adrenal glands from making androgens include ketoconazole and aminoglutethimide; and orchiectomy is surgery to remove the testicles, the main source of male hormones, to decrease hormone production. Hot flashes, impaired sexual function, and loss of desire for sex may occur in men treated with hormone therapy.

Deaths from prostate cancer are typically a result of metastasis of a prostate tumor. Therefore, early detection of the development of prostate cancer is critical in reducing mortality from this disease. Measuring levels of prostate-specific antigen (PSA) has become a very

common method for early detection and screening, and may have contributed to the slight decrease in the mortality rate from prostate cancer in recent years. Nowroozi, et al. (1998) Cancer Control 5:522-531. However, many cases are not diagnosed until the disease has progressed to an advanced stage.

Prognosis, Outcome

Prognosis is typically recognized as a forecast of the probable course and outcome of a disease. See Dorland's Medical Dictionary. As such, it involves inputs of both statistical probability, requiring numbers of samples, and outcome data. Herein, outcome data is utilized in the form of prostate cancer recurrence after RP. A patient population of many dozens is included, providing statistical power.

The ability to determine which cases of prostate cancer will respond to treatment, and to which type of treatment, would be useful in appropriate allocation of treatment resources. As indicated above, the various standard therapies have significantly different risks and potential side effects. Accurate prognosis would also minimize application of treatment regimens which have low likelihood of success. Such also could avoid delay of the application of alternative treatments which may have higher likelihoods of success for a particular presented case. Thus, the ability to evaluate individual prostate cases for markers which subset into responsive and non-responsive groups for particular treatments are very useful.

Current models of prostate cancer classification are poor at distinguishing between tumors that have similar histopathological features but vary in clinical course and outcome. Kattan, et al. (1998) J. Nat'l Cancer Inst. 90:766-771; and Kattan, et al. (1999) J. Clin. Oncol. 17:1499-1507. Identification of novel prognostic molecular markers is a priority if radical treatment is to be offered on a more selective basis to those prostate cancer patients with clinically significant disease. A novel strategy is described to discover molecular markers for prostate cancer prognosis by assessing genome-wide gene expression in many localized prostate cancers and modeling these data based on each patient's known clinical outcome and preoperative serum prostate-specific antigen concentration. The study herein is directed to molecularly define different forms of prostate cancer which can translate directly into prognosis. And such prognosis allows for application of a treatment regimen having a greater statistical likelihood of cost effective treatments and minimization of negative side effects from the different treatment options.

Prostate cancer biopsy samples were collected and analyzed for gene expression across most genes of the human genome. Among genes detected at appropriate levels, correlations with outcome data were evaluated. Genes whose expression levels correlated with statistical significance to outcome data were identified.

This approach identified about 270 genes that demonstrated a strong association ($P < 0.01$) with disease outcome, e.g., prostate cancer relapse, and were superior in their predictive ability relative to prostate-specific antigen levels, one of the standard markers. One of these genes, the putative calcium channel protein trp-p8, is androgen-regulated and loss of *trp-p8* appears to be associated with aggressive disease. The findings provide a method of survival analysis of gene expression profiles of cancers with censored follow-up data and identify novel molecular markers of prostate cancer progression with strong predictive power that may be used to select prostate cancers with an aggressive phenotype.

Thus, the invention herein provides statistical correlations of marker expression in appropriate samples with disease outcome.

Survival Analysis

The present invention provides the application of classical multivariable survival analysis to a prostate cancer microarray data set incorporating the expression profiles of over 46,000 genes, to identify markers of disease outcome. This technique provides several significant advances over previous methods of analyses that have been used to discover markers of disease outcome from microarray data. In contrast to previously described statistical methods that rely on the classification of tumors based on known outcome (18) or known classifiers of patient outcome (eg. estrogen receptor status) (19, 20), this technique provides for censored data. This enables these analyses to proceed prior to the occurrence of all events, in this case, PSA relapse. Moreover, this survival analysis incorporates the time taken to PSA relapse and may also include covariates (eg. preoperative serum PSA levels) in order to identify genes that provide additional predictive value above conventional markers of outcome. The statistical analyses described herein have also incorporated a stringent method of estimating the pFDR that was recently described (10). This method is designed specifically for the analysis of microarray data where general dependence between hypotheses or "clumpy dependence" exists, where 50 or more genes interact in common pathways to produce some overall process (10). However, this is the first instance that it has been applied to microarray data from a survival analysis.

A recently published analysis to discover new markers of prostate cancer outcome utilized microarray analyses of prostate cancers to classify small groups of tumors where the recurrence status was known (21). That study found that no single gene was statistically associated with recurrence at $P < 0.05$ and instead adopted a 5-gene model that most commonly included chromogranin A and inositol triphosphate receptor 3 (IP3R). The significant differences between our study and these previously published data are (1) our adoption of a Cox proportional hazards model, and (2) our observation that 277 individual genes were predictive for prostate cancer relapse, none of which overlapped with the genes in the 5-gene model identified by Singh *et al.* (2002). There are two prevailing explanations for the latter discrepancy. Firstly, the number of genes interrogated by oligonucleotide microarrays in our study was 4-fold greater; *trp-p8* is an example of a gene which was not present in the oligonucleotide array used in the previous study. As a result, the genes identified by Singh *et al.* (2002), were associated with *P* values of less significance than those presented in Tables 1 and 2. Secondly, by utilizing a statistical method that applies to censored data, we were able to take into account the varying times to prostate cancer relapse in this model. Therefore, we were able to use our full data set in the analysis, rather than restricting the analysis to those patients with a specified length of follow-up. The larger data set and concomitant increase in statistical power may also contribute to our results differing from those of Singh *et al.*

The TRP channels are made of subunits with six membrane-spanning domains with both carboxy and amino termini located intracellularly that probably form into tetramers to form non-selective cationic channels, which allow for the influx of calcium ions into the cell. Trp-p8 or TRPM8 is a member of the TRPM subfamily of TRP ion channels that have potential roles in Ca^{2+}-dependent signaling, control of cell cycle proliferation, cell division and cell migration. Ligand binding to some membrane receptors initiates a sequence of events that lead to the activation of phospholipase C, generating inositol-1,4,5-triphosphate which opens the intracellular ion channel IP3R and liberates Ca^{2+} from the endoplasmic reticulum. Activation of the TRP channels accompanies this chain of events, allowing the influx of calcium ions into the cells, although their activation is not necessarily directly linked to Ca^{2+} depletion from internal stores (22). Calnexin, which is also identified in this analysis as a marker of potential prognostic utility ($P = 0.004$), is believed to be a key chaperone involved in the folding, assembly and oligomerization of newly synthesised IP3R receptors (24). Thus, our study implicates an important role for the phosphatidylinositol signal transduction.

Our observation that loss of *trp-p8* is associated with a poor prognosis is also reminiscent of the prognostic role of another of the TRPM subfamily, TRPM1 or melastatin, in melanoma. Downregulation of melastatin mRNA in primary cutaneous melanoma is a prognostic marker for metastasis in patients with localized melanoma and is independent of conventional clinicopathological predictors of metastases (25). Recent studies showed that the rat (26) and mouse (27) orthologues of trp-p8 are functional calcium channels that respond to cold stimuli. Although cold is unlikely to be the natural stimulus for trp-p8 in the prostate, the implication that the human trp-p8 protein may be a functional Ca^{2+} channel suggests a role in the regulation of intracellular Ca^{2+} levels with possible effects on cell motility, cell proliferation and resistance to apoptotic stimuli.

In summary, our analyses have identified a group of genes that strongly correlate with prostate cancer relapse and contribute unique information to relapse prediction above preoperative PSA.

Prognosis Determination

One application of the survival analysis results is to generate a prognostic test for prostate cancer. First, we use TAQMAN® analysis to determine the absolute levels of prognostic genes in 75-150 or more prostate cancer patients. Then we correlate the absolute levels of the prognostic genes with patient outcome by a statistical analysis and determine threshold levels of prognostic genes; from which we establish a profile of the threshold level of each prognostic gene associated with a good outcome. For determining the prognosis of a prostate cancer patient, the absolute level of one or more prognostic genes of this patient is determined. Then the absolute level of one or more prognostic genes of this patient is compared with the above established threshold values. Absolute level higher (or lower depending on the prognostic gene) than the threshold values indicates good outcome.

The normalized quantitative level of absolute gene expression of a prognostic gene, from which outcome is predicted, is determined first. Quantitative polymerase chain reaction (PCR)-based methods can be applied. RT-PCR (reverse transcriptase PCR) primers are designed for selected prognostic genes, in order to perform a TaqMan® analysis.

TAQMAN® analysis is a real-time quantitative PCR, which is a powerful method used for gene expression analysis, genotyping, pathogen detection/quantitation, mutation screening and DNA quantitation. See, e.g., Bartlett (2003) PCR Protocols (2^d ed.) Humana Press; and

O'Connell (2002) RT-PCR Protocols, Humana Press. The technology uses, e.g., an ABI Prism instrument (TAQMAN®) to detect accumulation of PCR products continuously during the PCR process thus allowing easy and accurate quantitation in the early exponential phase of PCR. The basis for PCR quantitation in the ABI instrument is to continuously measure PCR product accumulation using a dual-labeled flourogenic oligonucleotide probe called a TAQMAN® probe. This probe is composed of a short (ca. 20-25 bases) oligodeoxynucleotide that is labeled with two different flourescent dyes. On the 5' terminus is a reporter dye and on the 3' terminus is a quenching dye. This oligonucleotide probe sequence is homologous to an internal target sequence present in the PCR amplicon. When the probe is intact, energy transfer occurs between the two flourophors and emission from the reporter is quenched by the quencher. During the extension phase of PCR, the probe is cleaved by 5' nuclease activity of Taq polymerase thereby releasing the reporter from the oligonucleotide-quencher and producing an increase in reporter emission intensity. The laser light source excites each well and a CCD camera measures the fluorescence spectrum and intensity from each well to generate real-time data during PCR amplification. The ABI Prism software examines the fluorescence intensity of reporter and quencher dyes and calculates the increase in normalized reporter emission intensity over the course of the amplification. The results are then plotted versus time, represented by cycle number, to produce a continuous measure of PCR amplification. To provide precise quantification of initial target in each PCR reaction, the amplification plot is examined at a point during the early log phase of product accumulation. This is accomplished by assigning a fluorescence threshold above background and determining the time point at which each sample's amplification plot reaches the threshold (defined as the threshold cycle number or CT). Differences in threshold cycle number are used to quantify the relative amount of PCR target contained within each tube as described previously.

The TAQMAN® primers are designed within the open-reading frame of the prognostic gene of interest so that the amplicon averages 80 bp. Prostate tissue samples from 70-150 or more prostate cancer patients with known histories are collected and RNA is extracted from these samples using standard methods. TAQMAN® analysis is performed on these samples for the appropriate genes. Using the TAQMAN® analysis, the normalized absolute levels of the prognostic genes are then correlated with patient outcome. Using statistical analyses the threshold level of gene expression, which predicts outcome, is then determined. Subsequent patient samples can then be analyzed for potential of relapse and the physician can better define

the patient treatment based on whether the patient is predicted to relapse. Subsetting of the data into various outcomes is achieved through statistical analyses. (Snedecor and Cochran (1994) Statistical Methods (8th ed.) Iowa State University Press; and Duda, et al. (2001) Pattern Classification (2d ed.) Wiley and Sons.)

Genes, Markers, Kits

The present study provides specific identification of multiple genes whose expression levels in biological samples will serve as markers to evaluate prostate cancer cases. These markers have been selected for statistical correlation to disease outcome data on a large number of prostate cancer patients.

The expression levels of these markers in a biological sample may be evaluated by many methods. They may be evaluated for RNA expression levels. Hybridization methods are typically used, and may take the form of a PCR or related amplification method. Alternatively, a number of qualitative or quantitative hybridization methods may be used, typically with some standard of comparison, e.g., actin message. Alternatively, measurement of protein levels may performed by many means. Typically, antibody based methods are used, e.g., ELISA, radioimmunoassay, etc., which may not require isolation of the specific marker from other proteins. Other means for evaluation of expression levels may be applied upon purification of the marker. Antibody purification may be performed, though separation of protein from others, and evaluation of specific bands or peaks on protein separation may provide the same results. Thus, e.g., mass spectroscopy of a protein sample may indicate that quantitation of a particular peak will allow detection of the corresponding marker. Multidimensional protein separations may provide for quantitation of specific purified entities.

Tables 1A-C describe markers of the invention useful for the prognosis of prostate cancer.

Table 1A shows radical prostatectomy samples that were analyzed using the Eos Hu03 GENECHIP®, which contains 59680 probesets. Each probeset's intensity measure was entered as a continuous explanatory variable in a Cox proportional hazards regression survival analysis predicting relapse. Pretreatment PSA concentration was entered as a predictor in each analysis. The interquartile range hazard ratio (IQR HR) for each probeset was then calculated. This approach was used since in conventional Cox proportional hazards analyses, the hazards ratios

for a covariate are computed by raising e, the base of natural logarithms, to the power of its regression coefficient. However, because the expression data are treated here as continuous covariates, hazards ratios expressed in this manner illustrate only the change in risk of relapse associated with a change of 1 unit on the expression scale, a change too small to be meaningful. To put the hazard ratios and associated confidence limits on a more interpretable scale, presented here is the hazards ratio associated with a change in expression values equivalent to 1 interquartile range (IQR) of the sample data for each probeset. The IQR is simply the 75th percentile minus the 25th percentile, and thus contains the middle 50 percent of observations. From this analysis, 266 probesets were found to be significant predictors of relapse at $P < 0.01$.

Table 1B lists the accession numbers for Pkey's lacking UnigeneID's for table 1A. For each probeset is listed the gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 1C shows genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 1A. For each predicted exon, is listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 1A:

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
p value: p value for relapse prediction (see Table 1A description)

Pkey	ExAccn	UnigeneID	Unigene Title	p value
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.80177E-05
439785	AA845608	Hs.132860	ESTs	0.000106034
413924	AL119964	Hs.75616	seladin-1	0.000157824
459680	H96982	Hs.42321	ESTs	0.00019382
431542	H63010	Hs.5740	ESTs	0.000250668
404824			C22000161*:gi|2443331|dbj|BAA22375.1| (D	0.000290214
446021	BE389213	Hs.286	ribosomal protein L4	0.000320882
434999	AW975059		gb:EST387164 MAGE resequences, MAGN Homo	0.000341555
458509	AA654650	Hs.282906	ESTs	0.000351184
406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	0.000536315

	423381	BE250014		gb:600943007F1 NIH_MGC_15 Homo sapiens c	0.000602528
	419037	R39895	Hs.257391	hypothetical protein DKFZp761J1523	0.00065526
	414898	AA157726	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.000707085
	404582			Target Exon	0.00074185
5	458607	AV656002		ESTs, Moderately similar to unnamed prot	0.000805762
	402861	D14661		Wilms' tumour 1-associating protein	0.000870602
	441494	AW452344	Hs.129977	ESTs	0.000875883
	452753	AA028049	Hs.277728	SEC14 (S. cerevisiae)-like 2	0.000934337
	422516	BE258862	Hs.117950	multifunctional polypeptide similar to S	0.000969694
10	443675	AI081397		ESTs	0.000984435
	425297	AA354685		gb:EST63062 Jurkat T-cells V Homo sapien	0.001036315
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	0.001065289
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	0.00111943
	438611	AW204707	Hs.123387	ESTs	0.001135255
15	434949	AW976087		ESTs, Highly similar to AF161437 1 HSPC3	0.001142057
	430845	AF024690	Hs.248056	G protein-coupled receptor 43	0.001172874
	429446	AI547111		gb:PN2.1_A01_G12.r mynorm Homo sapiens c	0.001185816
	444773	BE156256	Hs.11923	hypothetical protein	0.001200592
	446702	R44518	Hs.143496	ESTs	0.001311934
20	415179	D80630		gb:HUM091D02B Human fetal brain (TFujiwa	0.0013887
	448479	H96115	Hs.21293	UDP-N-acteylglucosamine pyrophosphorylas	0.001402576
	430799	C19035	Hs.164259	ESTs	0.001404901
	454930	AW845987	Hs.68864	ESTs, Weakly similar to phosphatidylseri	0.001417466
	407241	M34516		gb:Human omega light chain protein 14.1	0.001504145
25	421970	AF227156	Hs.110103	RNA polymerase I transcription factor RR	0.001519398
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	0.001610938
	400207			Eos Control	0.00161581
	423318	AW467064	Hs.5740	ESTs	0.001622161
	413102	AI199981	Hs.109694	ESTs, Weakly similar to T27691 hypotheti	0.001683835
30	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	0.001688301
	419872	AI422951	Hs.146162	ESTs	0.001710345
	402812			NM_004930*:Homo sapiens capping protein	0.001742994
	427418	AA402587		LAT1-3TM protein	0.001743363
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	0.001830512
35	457397	AW969025	Hs.109154	ESTs	0.001994494
	403372	AW249152		sirtuin (silent mating type information	0.002012497
	415344	T65456		gb:yc73a11.r1 Soares infant brain 1NIB H	0.002025172
	422017	NM003877	Hs.110776	STAT induced STAT inhibitor-2	0.002053043
	406554			Target Exon	0.002105231
40	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	0.002151173
	407040	X03689		gb:Human mRNA fragment for elongation fa	0.002199926
	419657	AK001043	Hs.92033	integrin-linked kinase-associated serine	0.002290654
	457662	AA907734	Hs.124895	ESTs	0.002413693
	447308	AI005334	Hs.22015	ESTs, Weakly similar to I38344 titin, ca	0.002472822
45	420707	BE312807	Hs.143407	ESTs, Weakly similar to A54849 collagen	0.002479439
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	0.00251185
	429289	AI400746	Hs.62187	phosphatidylinositol glycan, class K	0.002513019
	454275	AW293900	Hs.304842	ESTs, Weakly similar to AMYH_YEAST GLUCO	0.002559888
	408603	R25283	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	0.002571063
50	434614	AI249502	Hs.29669	ESTs	0.002629652
	406558			C5000893:gi|6226859|sp|P38525|EFG_THEMA	0.002723963
	440325	NM003812	Hs.7164	a disintegrin and metalloproteinase doma	0.002768837
	440518	AA888046	Hs.233235	ESTs	0.002805131
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	0.002848507
55	421655	AA464812		gb:zw63h05.r1 Soares_total_fetus_Nb2HF8_	0.002855486
	445375	AW779857	Hs.166987	ESTs, Weakly similar to B35363 synapsin	0.002861874
	456647	AI252640	Hs.110364	peptidylprolyl isomerase C (cyclophilin	0.002867794
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	0.002897453
	430389	AL117429	Hs.240845	DKFZP434D146 protein	0.002920262
60	423479	NM014326	Hs.129208	death-associated protein kinase 2	0.00294831
	443884	N20617	Hs.194397	leptin receptor	0.002997251
	457926	AA452378		Homo sapiens mRNA; cDNA DKFZp547J125 (fr	0.003054911
	459710	AI701596	Hs.121592	ESTs	0.003061123

	404560			Target Exon	0.003092402
	438657	AI141396	Hs.158741	ESTs	0.003131957
	400282			NM_005313:Homo sapiens glucose regulated	0.003134356
	416144	AA381556	Hs.331803	heat shock 60kD protein 1 (chaperonin)	0.003162736
5	430677	Z26317		desmoglein 2	0.003170664
	423562	AJ005197	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	0.003217503
	401040			C11000425:gi|4507721|ref|NP_003310.1| ti	0.003244184
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	0.003251143
	415439	R21114	Hs.21383	ESTs	0.003317352
10	458054	AW979052	Hs.5734	meningioma expressed antigen 5 (hyaluron	0.003355436
	435346	AI248389	Hs.188105	ESTs	0.00337758
	410452	AW749026		gb:RC3-BT0319-100100-012-b05 BT0319 Homo	0.003407284
	427548	AA813784	Hs.123001	ESTs	0.003456322
	438918	AI126484	Hs.127486	ESTs	0.00347913
15	448076	AJ133123	Hs.20196	adenylate cyclase 9	0.003583335
	420339	AW968259	Hs.186647	ESTs	0.003607275
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	0.003628615
	452143	N29649	Hs.260855	Homo sapiens cDNA: FLJ21410 fis, clone C	0.003701377
	422813	AV656571	Hs.121068	transmembrane 4 superfamily member 6	0.00379349
20	401524			Target Exon	0.003793904
	453768	BE382670	Hs.198511	Homo sapiens mRNA; cDNA DKFZp7611177 (fr	0.003810346
	424954	NM000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	0.003826169
	440409	AW294316	Hs.125608	ESTs	0.003879241
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	0.003898535
25	444756	AA278501	Hs.200332	hypothetical protein FLJ20651	0.003922529
	429769	NM004917	Hs.218366	kallikrein 4 (prostase, enamel matrix, p	0.003947007
	443403	R01027	Hs.133560	ESTs	0.003959306
	400219			Eos Control	0.003966793
	448489	AI523875		gb:tg97d04.x1 NCI_CGAP_CLL1 Homo sapiens	0.004120703
30	428378	AA427571	Hs.98531	ESTs	0.004121896
	449909	AA004681	Hs.59432	ESTs	0.004158168
	425127	AW841272	Hs.330418	Homo sapiens cDNA: FLJ22459 fis, clone H	0.004166839
	427485	AF039652	Hs.178655	ribonuclease H1	0.004198226
	416305	AU076628	Hs.79187	coxsackie virus and adenovirus receptor	0.004214942
35	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	0.00422178
	414091	T83742	Hs.334616	gb:yd67g02.s1 Soares fetal liver spleen	0.004236934
	446415	T27097	Hs.22790	ESTs	0.004250994
	407218	AA095473	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo	0.004267222
	436626	W35362	Hs.103012	ESTs	0.00432651
40	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	0.004332167
	409841	AW502139		gb:UI-HF-BR0p-ajr-e-05-0-UI.r1 NIH_MGC_5	0.004357117
	423022	AA320525	Hs.201076	ESTs	0.004401104
	429332	AF030403	Hs.199263	Ste-20 related kinase	0.004405129
	417834	BE172058	Hs.82689	tumor rejection antigen (gp96) 1	0.004424022
45	419808	AW008030	Hs.337536	Homo sapiens cDNA: FLJ21568 fis, clone C	0.004471786
	450088	AW292933	Hs.254110	ESTs	0.004491465
	431151	BE207083		gb:ba10d10.y1 NIH_MGC_7 Homo sapiens cDN	0.00450798
	431281	AW970573		gb:EST382654 MAGE resequences, MAGK Homo	0.004657684
	420960	Z45662	Hs.90797	Homo sapiens clone 23620 mRNA sequence	0.004798622
50	409540	AW409569	Hs.101550	gb:fh01e09.x1 NIH_MGC_17 Homo sapiens cD	0.004819322
	456643	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	0.004821217
	449889	AA004613	Hs.168672	ESTs	0.004888264
	413074	AI871368	Hs.8417	hypothetical protein DKFZp761M0423	0.004890295
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	0.004925393
55	434263	N34895	Hs.44648	ESTs	0.004967084
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	0.004996569
	435981	H74319	Hs.188620	ESTs	0.005005242
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	0.005047202
	414916	AA206991		high-mobility group (nonhistone chromoso	0.005130846
60	434855	AA765019	Hs.191850	ESTs	0.005199586
	406651	AI559224		gb:tq32c02.x1 NCI_CGAP_Ut1 Homo sapiens	0.005212356
	440675	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	0.005249269
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	0.005270232

	400487			ENSP00000238977*:Interferon-induced prot	0.005353963
	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	0.005371997
	410054	AL120050	Hs.58220	Homo sapiens cDNA: FLJ23005 fis, clone L	0.005404329
	409344	R47279	Hs.285673	hypothetical protein FLJ20950	0.005429984
5	421215	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypotheti	0.005442884
	450661	AW952160		ESTs	0.005447857
	424269	AW137691	Hs.104696	ESTs	0.005483308
	412294	AA689219		poly(A)-binding protein, nuclear 1	0.005530138
	404511			NM_004349:Homo sapiens core-binding fact	0.005558982
10	437006	AW976322	Hs.291561	ESTs	0.005639929
	432989	NM014074		PRO0529 protein	0.00572161
	417584	AA252468	Hs.1098	DKFZp434J1813 protein	0.005734515
	437992	AW450086	Hs.145989	ESTs, Highly similar to DHHC-domain-cont	0.005769051
	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	0.005799441
15	420929	AI694143	Hs.296251	programmed cell death 4	0.00585145
	415121	D60971	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	0.005963023
	404662			Target Exon	0.006001874
	445878	AI262974	Hs.145587	ESTs	0.006055258
	421090	BE301870	Hs.101813	solute carrier family 9 (sodium/hydrogen	0.006079413
20	405155			Target Exon	0.006110052
	427379	D79254	Hs.256066	ESTs	0.006133565
	412561	NM002286	Hs.74011	lymphocyte-activation gene 3	0.006142277
	434257	AF121255	Hs.193053	eukaryotic translation initiation factor	0.006144213
	400141			Eos Control	0.006200101
25	453359	AA448787	Hs.24872	ESTs	0.006315475
	433151	AW973735	Hs.17631	hypothetical protein DKFZp434E2135	0.006324267
	449791	AI248740	Hs.133323	ESTs	0.006355539
	405722	BE410124		NM_021120:Homo sapiens discs, large (Dro	0.006388997
	427527	AI809057	Hs.293441	immunoglobulin heavy constant mu	0.006397862
30	411487	AF116666	Hs.70333	hypothetical protein MGC10753	0.006474544
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	0.00651405
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	0.006535001
	443425	AI056776	Hs.133397	ESTs, Weakly similar to I78885 serine/th	0.006574089
	409179	BE062633	Hs.28338	KIAA1546 protein	0.006647277
35	431947	AL359613	Hs.49933	hypothetical protein DKFZp762D1011	0.006663987
	402339			NM_003425*:Homo sapiens zinc finger prot	0.006744987
	422262	AL022315	Hs.113987	lectin, galactoside-binding, soluble, 2	0.006803463
	404458			CX000877*:gi|11877268|emb|CAC18893.1| (A	0.006816499
	431693	AI459519		serine (or cysteine) proteinase inhibito	0.006849491
40	428734	BE303044	Hs.192023	eukaryotic translation initiation factor	0.00696046
	444204	AI129194	Hs.143040	ESTs	0.007032748
	406837	R70292	Hs.156110	immunoglobulin kappa constant	0.007051544
	442482	NM014039	Hs.8360	PTD012 protein	0.007051611
	412006	AW451618		ESTs	0.00705506
45	435354	AA678267	Hs.117115	ESTs	0.007095576
	403505	M97639		receptor tyrosine kinase-like orphan rec	0.007139282
	451946	AI824901	Hs.281012	ESTs, Highly similar to strong homology	0.007271734
	433339	AF019226	Hs.8036	glioblastoma overexpressed	0.007286776
	436924	AA741001	Hs.326006	ESTs	0.007312314
50	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	0.007346563
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	0.007352833
	434256	AI378817	Hs.191847	ESTs	0.00736484
	439778	AL109729	Hs.99364	putative transmembrane protein	0.0073683
	423443	AI432601	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	0.007425186
55	405293			Target Exon	0.007457507
	426357	AW753757	Hs.12396	gb:RC3-CT0283-271099-021-a08 CT0283 Homo	0.007488395
	422921	BE062045		Homo sapiens cDNA: FLJ23260 fis, clone C	0.007499187
	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig),	0.007512156
	426091	BE544541	Hs.249495	heterogeneous nuclear ribonucleoprotein	0.007576069
60	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	0.007594318
	449787	AA005341	Hs.283559	ESTs	0.007675199
	412162	AA100600	Hs.69192	gb:zn63b10.s1 Stratagene HeLa cell s3 93	0.007681586
	413522	BE145897		gb:MR0-HT0208-221299-204-b07 HT0208 Homo	0.007824405

	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	0.007843962
	414586	AA306160	Hs.76506	lymphocyte cytosolic protein 1 (L-plasti	0.007931767
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	0.007975007
	404242			ENSP00000252213*:SODIUM BICARBONATE COTR	0.008032744
5	400206			Eos Control	0.008161865
	441011	AW137447	Hs.126408	ESTs	0.008169197
	449223	AB002348	Hs.23263	KIAA0350 protein	0.008169995
	451776	W45679	Hs.169854	hypothetical protein SP192	0.008174536
	418354	BE386973	Hs.84229	splicing factor, arginine/serine-rich 8	0.00821493
10	435188	AA669512	Hs.116679	ESTs, Weakly similar to A42826 T-cell le	0.00826337
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.008283276
	432981	NM002733	Hs.3136	protein kinase, AMP-activated, gamma 1 n	0.008309431
	433468	AA832055	Hs.170222	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.008310151
	457269	AI338993	Hs.134535	ESTs	0.00834154
15	431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	0.008414644
	426501	AW043782	Hs.293616	ESTs	0.008416828
	447623	AA350235	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	0.008419744
	429678	N70394	Hs.238956	ESTs	0.008452349
	444370	NM015344	Hs.11000	leptin receptor overlapping transcript-l	0.00847352
20	404557			C8001174*:gi|10432400|emb|CAC10290.1| (A	0.008502518
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	0.008537039
	441283	AA927670	Hs.131704	ESTs	0.008562466
	424640	AA344559	Hs.164428	ESTs	0.008568818
	452793	AW138760	Hs.61484	ESTs	0.008570907
25	420527	AA332287	Hs.175110	ESTs	0.00858412
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, l	0.008588847
	430316	NM000875	Hs.239176	insulin-like growth factor 1 receptor	0.008606329
	436524	AA922236	Hs.221037	ESTs	0.008616325
	444700	NM003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	0.008668985
30	441222	AI277237	Hs.44208	hypothetical protein FLJ23153	0.008703638
	429170	NM001394	Hs.2359	dual specificity phosphatase 4	0.008704913
	454393	BE153288		gb:PM0-HT0335-180400-008-c08 HT0335 Homo	0.008716471
	456107	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	0.008767147
	402091			Target Exon	0.008853214
35	409115	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	0.008866852
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	0.008901601
	428944	AA780181	Hs.41182	Homo sapiens DC47 mRNA, complete cds	0.008970935
	419052	T83291	Hs.220624	ESTs	0.008998014
	446203	Z47553	Hs.14286	flavin containing monooxygenase 5	0.009023814
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	0.009035339
	452264	AU077013	Hs.28757	transmembrane 9 superfamily member 2	0.009036494
	446425	AW295364	Hs.255418	ESTs	0.009058296
	446547	AI334965	Hs.176976	ESTs	0.009087495
	419555	AA244416		gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	0.009114049
45	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	0.009119167
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	0.009188183
	411950	T28407	Hs.81564	platelet factor 4	0.009188186
	457146	BE271371		biphenyl hydrolase-like (serine hydrolas	0.009228646
	454131	AI215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	0.009282618
50	404483			C8000657*:gi|1504040|dbj|BAA13219.1| (D8	0.009290064
	421351	AU076667	Hs.103755	receptor-interacting serine-threonine ki	0.00929738
	417963	AA210718	Hs.104157	ESTs, Weakly similar to KIAA0694 protein	0.009334158
	429011	AA443182	Hs.188835	ESTs	0.009370261
	425380	AA356389	Hs.32148	AD-015 protein	0.009402223
55	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	0.009446269
	424546	BE465173	Hs.194031	ESTs	0.009446339
	444524	AI160643	Hs.28332	Homo sapiens cDNA: FLJ21560 fis, clone C	0.009472535
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	0.009508794
	422669	H12402	Hs.119122	ribosomal protein L13a	0.00950994
60	420593	AA280356	Hs.187634	ESTs	0.009517511
	447502	AA312531	Hs.26471	Bardet-Biedl syndrome 4	0.0096083
	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fis, clone PL	0.009645426
	434401	AI864131	Hs.71119	Putative prostate cancer tumor suppresso	0.009778291

432826	X75363	Hs.250770	ACO for serine protease homologue	0.009849589
428840	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	0.009881804
413592	AA130654	Hs.302274	Homo sapiens cDNA FLJ12328 fis, clone MA	0.009899125
443102	AI247472	Hs.132965	ESTs	0.009964996

TABLE 1B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409841	1156088_1	AW502139 AW502432 AW502235 AW501683 AW502647
410452	1204142_1	AW749026 BE066111 T97135
412006	127108_1	AW451618 AA846096 AI004201 AI242026 N38791 AI032976 AA099469 N45423
412294	128797_2	AA689219 AI983045 T16928 Z45040 R20321
413522	1374614_1	BE145897 BE145816 BE145885
414916	15071_24	AA206991 BE564126 AA092392 AA090034 AA090545 AA093840 N84434 BE269369 AI535705 AI535744 AI535682 AF283771 H28296 H27400 BE618821 AI873907 BE622711 AI471738 AA557452 AA304303 AW794938 AA600212 AW027283 AW938645 AI654646 AA370554 AA356536 AA715713 N87841 AW575412 AA987424 AA319424 BE084055 AA827973 AA330422 AW630429 N38949 AA360952 AA045606 BE257213 AW768545 AA101746 AI335554 N26696 AI630155 AW170282 AA206705 AA357094 AW603120 AW793181 AI127978 AA639183 AW020136 BE536372 AA093946 AA730118 BE079411 T90564 D83849 D20752 W07682 BE540914 F22618 AI041775 AA196344 AA366696 AA083771 AA054783 AA330028 BE544267 AA247271 AW958331 BE073175 AW945457 AA229491 AW874401 R34185 R81133 W32781 AI191194 BE277231 W79255 AW800102 AI935842 AA928301 AA230310 AI742195 BE566990 AW673140 AI829489 AA054719 AW512749 AA782987 AI088142 AW103898 AA714697 AW574795 AI056134 AW162373 BE148890 AW068721 AW076120 AA563764 AW016252 AW016253 AI338171 AI085967 AI338788 BE542084 AI186025 AI963188 AW079946 AI034040 AI961313 AI831345 N79755 AA029435 AA910600 AA618386 AI336429 AA230308 AI346567 AA541647 AW024986 AI926174 AA878167 AW026237 AA668251 W15170 AA129635 AI363729 AA309687 AI453176 AI282417 H89557 AW264978 D55190 AA188911 AI471512 AI537126 AW675575 AI673287 AI476121 AA563901 AA353344 N93269 N80559 L13805 AA564621 AI056119 AI587020 AW874624 AI803890 AW074286 AA745955 AW152331 AI282228 AI081139 AI147252 AI126996 AI970694 D55874 AA313759 AW023735 AA999920 AI285652 AI476553 AI252804 AI096960 AW151090 AA876366 W32423 D57151 AA856637 AI954376 W73923 AL047978 BE041344 AA861867 AI346526 AL047979 AI348036 AI187244 AA328683 AA197248 N72984 AA862752 AA747207 AA876587 AA845496 AA890470 AW170401 AI127224 N99881 AW074379 AA938114 AI197777 AI753834 AI346536 AA331597 AI367738 AA977063 W93785 AA872167 AI932924 AA614560 AI434283 AI160153 AW130136 BE542026 AA385117 AA130703 AA778269 AI769329 AI285034 AW340835 AI224601 AA663430 AA846183 AI362627 AA903448 AW238760 AI283178 AV662138 AI138363 AA860743 AI368179 AI280190 AI139131 AI359157 H99812 AA771749 AI539068 AI089843 AI566789 AI281240 AI352354 AI769243 AI092187 AI073627 AI473623 AW276039 AI798397 AI024587 AA889467 AI683918 AW673268 AA602941 AA861823 AA668586 AA772542 AI077928 AA594116 AI018648 AI421799 AA705955 AA586855 AA577106 AI131297 AI355412 AI350882 AW265014 AW043934 AI127696 AW469864 AI041801 AL048264 AA961777 AI246050 AA566002 AI469308 AA809086 AW768947 AA507781 AI361342 AI368477 AA133897 AI300444 AI768467 AA773978 AW062352 AA648130 AA827606 AI094950 T61248 AA101747 AI348251 AI092294 AA565522 T39158 W33201 C75489 AA670425 AA483085 R48684 T28966

H96803 AA641999 AA709360 H99805 T19371 AW879059 AA524370 AW338262 N72895 AW591714 T63777 AL047945 AA150131 AA146973 AW878989 AA877803 T56122 AA147065 AA342484 AA342236 AW270920 AI913364 AW795486 AI865002 W94286 AA209325 T40443 AI268918 AI418552 T48135 M62207 AA328164 AW795480 BE169953 BE169983 AA206888 AA132394 AW149866 T57929 W15510 C75674 R81132 AI423687 AI193465 H28297 AA994473 F04357 BE243460 AA987347 AI376779 AA927274 T03381 H99134 T03851 AA384714 AW265058 BE041328 BE541757 AI910675 T64485 N89843 AA688338 T64628 AI143530 AI026855 F03043 AA865434 AA363018 AA459233 AA664746 N68567 AW467363 T16030 AW149914 AA994312 BE350136 AA307427 AI658528 L13804 AA384004 N71219 N22172 AW364964

415179 1527481_1 D80630 D80896 D80895

415344 1534510_1 T65456 F11749 Z43023 F06216 R18181 R17246

419555 185884_1 AA244416 AA244401

419733 187589_1 AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002 AA295134 AW188870 H75644 AA526037 AA347970 AW961788 H61476 AL133779 AA449282 H28581 AA249370

421655 204993_1 AA464812 AA431899 AA295193 AW959241

422921 222939_1 BE062045 Z43804 W35143 AI761615 N33753 BE062044 BE551229 AI088004 N33865 AA332473 AA374196 N48481

423381 227731_1 BE250014 BE293608 BE252781 AA325222 AW904396

425297 249704_1 AA354685 AW962101 H85269 F11427 R55281

427418 278594_1 AA402587 AI760178 AI911270 AI184927 AI277654 AA402398 AI633280 AW002589 AI984968 AI810234 AI671725 AI419580 AA705629 AW138044 AI719961 D45607 AA455831

429446 304683_1 AI547111 AW973749 AA558007

430677 3216_1 Z26317 NM_001943 AW991316 BE018413 AW996800 AW996267 AW996264 W73983 AA313797 BE513193 AW861416 AW857494 AA488331 BE171045 AW366926 BE002219 AW996792 AW753487 AW361908 BE003946 AW858751 AW858747 AW858750 AW858755 AW858749 D58979 AW363740 AW859003 AW363742 AW858999 AW471344 BE072891 AW753745 BE395396 AI378517 D58730 AW748942 BE395765 BE153312 BE153169 BE153241 AW371849 AW371853 AW748956 AA506621 AA723159 AI933746 AW473996 AW572140

431151 328652_-1 BE207083

431281 330904_1 AW970573 AA501880 AA501870

431676 336411_1 AI685464 AW971336 AA513587 AA525142

431693 33663_3 AI459519 AI366092 AF121175 AL042956 F11899 AI436382 AI133591 AI675879 AA081306 AI948730 BE243645 AA448957 H09862 AI382265 N92723 AL048959 AI356415 BE245782 AI288626 AI949306 AI814412 AW207026 AI659678 AI984766 AA741391 AI453490 AW166423 AI799883 AL045697 AI826075 AI952039 AA167742 BE463776 R01203 AI972947 AI623819 AW167132 AW337996 AW264027 AA209462 AI863491 T65400 AI394192 R62397 AW968250 BE464852 AW474624 AI758979 AW474705 BE046016 AI949348 AI289432 AI620722 AW440580 AI610824 AI458169 AW002172 AI634183 AA648408 AI289435 C00469 R62398 AI287482 H24845 F09546 AI125609 W93405 AA150039 AA150203 H09775 AI951377 AI631154 AA258738 AA744971 AA449685 AI434048 AA167836 R01316 T54772

432989 35719_1 NM_014074 AF111848

434949 39603_1 AW976087 AA100561 AF161437 D30850 AA767385 AI990080 AI337209 AA086348 AW002909 AA747908 AW450816 AW361653 BE145974 BE146300 AW292658

434999 397353_1 AW975059 AA659177 AA733194

443675 577019_1 AI081397 N94610 AI633993 AW949183 W23817 AW297357 H17610 F32559

448489 765247_1 AI523875 R45782 R45781

450661 84193_1 AW952160 AI819147 AA774089 AA010589 AA319638 AI954753 AI634083 H39119 AA812766

454393 115888_1 BE153288 BE153151 BE152925 AA078302

457146 29193_1 BE271371 NM_004332 X81372 AI167945 AW071802 AI818871 AI017491 AA421820 AA558952 AA910750 AA973795 R54850 AI672895 AI418120 AI268326 AA911487

		AA167197 N46097 X57653 R10551 T28159 AA167111 AW840204 AW276222 R09405 N46098 AA284554 AW129121
457926	43767_1	AA452378 AL390181 H05571 R53363 R55079 R11987 R11919 R84811 R19546 AA046904 R22842 AL134431 F11225 W79925 H10691 AA354088 AW965695 AI198775 AI803682 AA040404 AI150653 AA040266 AI436656 AW575893 AI703024 AA446858 AI805847 AI699312 AW575924 R55051 R53965 R39826 AW772031 AA975258 AW901905 R43388 BE218163 AI074604 AI148281 AA758256 BE501159 H11032 AW131553 F08888 AW341569 AI347996 AI952708 AI374835 AI089094 AI284927 W74206 AI027303 AI274177 AW299757 AI377712 AW300882 AA883979 AI239912 AI346165 AA947211 R46050 AI698833 AA452150 R43898 AA904733
458607	65602_1	AV656002 AV655810

TABLE 1C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400487	8919452	Plus	19369-20782
401040	7232177	Plus	17623-17919
401524	7770429	Plus	34644-35263
402091	8117554	Minus	190-306
402339	7459859	Minus	24698-26511
402812	6010110	Plus	25026-25091,25844-25920
402861	2814366	Minus	14933-15231,15387-15627
403372	9087278	Minus	130002-130131
403505	7577651	Plus	11059-11541
404242	5672600	Minus	22722-22897,23164-23433
404458	7770571	Minus	35710-36276
404483	8096904	Minus	162212-163710
404511	8151864	Minus	148501-148659
404557	7243881	Minus	88508-88699
404560	8954219	Plus	29247-29437
404582	9739220	Plus	53230-53424
404662	9797105	Minus	99466-99713
404824	6478944	Plus	209436-209545,209741-209850
405155	9966228	Plus	130469-130723
405293	3845419	Minus	16255-16535,16665-17340
405722	9800078	Plus	140732-140892,141099-141268,141434-141714,142048-142192
406554	7711566	Plus	106956-107121
406558	7711569	Minus	14052-14190

Note: the ExAccn number of NM_ is abbreviated to NM in Table 1A-C.

Table 2 lists the first 50 genes, ranked by *P* value, identified by survival analysis to be associated with prostate cancer relapse.

Table 2

Rank	UniGene cluster	Genbank accession	Gene title	Risk of relapse[a]	*P*
1	Hs.189095	NM_020436	Sal-like 4	2.040	0
2	Hs.132860	AA845608	ESTs	0.341	0
3	Hs.75616	NM_014762	24-Dehydrocholesterol reductase (seladin-1)	0.293	0
4	Hs.42321	NM_173605	Hypothetical protein LOC283518	2.133	0
5	Hs.80667	NM_004726	RALBP1 associated Eps domain containing 2 (REPS2)	0.172	0
6	Hs.163543	NM_144704	Hypothetical protein FLJ30473	3.241	0
7	Hs.286	NM_000968	Ribosomal protein L4	0.215	0
8	Hs.114670	D49387	Leukotriene B4 12-hydroxydehydrogenase	2.380	0
9	Hs.366053	NM_024080	Transient receptor potential cation channel, subfamily M, member 8 (trp-p8)	0.260	0
10	Hs.366	AL389978	*Immunoglobulin heavy chain variable region*	2.436	0.001
11	Not available	BE250014	ESTs	0.295	0.001
12	Hs.257391	NM_032293	Hypothetical protein DKFZp761J1523	3.138	0.001
13	Hs.264330	AK024677	*N*-acylsphingosine amidohydrolase (acid ceramidase)-like	0.256	0.001
14	Hs.123468	NM_033225	CUB and Sushi multiple domains 1	0.185	0.001
15	Not available	AV656002	EST	0.251	0.001
16	Hs.129977	AW452344	ESTs	0.229	0.001
17	Hs.277728	NM_012429	SEC14-like 2	0.348	0.001
18	Hs.117950	NM_006452	Phosphoribosylaminoimidazole carboxylase	0.321	0.001
19	Hs.424973	BC018081	Clone IMAGE:4793702	0.225	0.001
20	Not available	AA354685	EST	0.363	0.001
21	Hs.356547	NM_138799	Hypothetical protein BC016005	0.337	0.001
22	Hs.7780	AL049969	cDNA DKFZp564A072	0.186	0.001
23	Hs.123387	AW204707	ESTs	0.375	0.001
24	Hs.377879	AK055649	cDNA FLJ31087 fis	3.112	0.001
25	Hs.248056	NM_005306	G protein-coupled receptor 43	0.211	0.001
26	Hs.301947	NM_014509	Kraken-like serine hydrolase	0.212	0.001
27	Hs.11923	NM_018982	Hypothetical protein DJ167A19.1	0.155	0.001
28	Hs.247423	NM_001617	Adducin 2 (β) (ADD2)	2.044	0.001
29	Not available	D80630	EST	2.753	0.001
30	Hs.21293	NM_003115	UDP-*N*-acteylglucosamine pyrophosphorylase 1	0.185	0.001
31	Hs.292859	C19035	ESTs, moderately similar to VPP2_HUMAN	2.375	0.001
32	Hs.68864	AW845987	Lipase, member H (LIPH), mRNA	0.273	0.001
33	Hs.405944	X57819	Ig λ chain	2.388	0.002
34	Hs.110103	NM_018427	RNA polymerase I transcription factor RRN3	0.337	0.002
35	Hs.256150	NM_080654	NY-REN-41 antigen	2.718	0.002
36	Hs.76847	NM_014610	α Glucosidase II alpha subunit	0.135	0.002
37	Hs.109694	AI199981	Oxysterol binding protein-like 8 (OSBPL8), mRNA	4.511	0.002
38	Hs.71119	NM_006765	Putative prostate cancer tumor suppressor (N33)	0.281	0.002
39	Hs.146162	AK075364	ESTs	2.151	0.002
40	Hs.333417	NM_004930	Capping protein (actin filament) muscle Z-line, β	0.291	0.002
41	Hs.410998	AA402587	ESTs, Highly similar to MLL septin-like fusion	1.507	0.002
42	Hs.79136	NM_012319	LIV-1 protein, estrogen regulated	0.210	0.002
43	Hs.109154	AW969025	ESTs	0.281	0.002
44	Hs.433622	NM_007085	Follistatin-like 1 (FSTL1)	0.233	0.002
45	Not available	T65456	EST	0.195	0.002
46	Hs.405946	NM_003877	Suppressor of cytokine signaling 2 (SOCS2)	0.448	0.002
47	Hs.127699	NM_001369	Dynein, axonemal, heavy polypeptide 5 (DNAH5)	0.284	0.002
48	Hs.422118	NM_001402	Eukaryotic translation elongation factor 1 alpha 1	0.175	0.002
49	Hs.92033	NM_030768	Integrin-linked kinase-associated serine/threonine phosphatase 2C	5.564	0.002
50	Hs.124895	AA907734	ESTs	3.399	0.002

[a] The risk of relapse is the IQR HR calculated for each probeset as described in "Materials and Methods."

Sequences described therein, where incomplete, may be extended either by informatics techniques, or by techniques of biochemistry and molecular biology. Many well known methods are available. See, e.g., Mount (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Ausubel, et al. (eds. 1999 and supplements) Current Protocols in Molecular Biology Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

Nucleic acid sequences are particularly described. Using linkages to publicly accessible databases, e.g., GenBank accession numbers, sequences are described whose presence or absence in the samples provides prognostic capacity. Correlations are made between the detection of such sequence and the outcomes of the prostate cancers. Thus, detection of physically linked, e.g., adjacent or contiguous, sequence will be equivalent. The correlation between presence of a 5' segment will be equivalent to such with a 3' segment of the same physical molecule.

The tables also provide protein sequences which correspond to the identified nucleic acid sequences. The amino acid embodiments of the markers will also exhibit similar correlations with outcome. Thus, the use of the protein embodiments can also be used in the invention. Proteins or fragments can be produced, and antibodies generated. See, e.g., Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press.

Kits for use in the prognostic methods are also made available. The kits will include reagents for detecting the markers, e.g., at the nucleic acid or protein level. Thus, for nucleic acid expression level prognosis kits, typically PCR primers or detectable hybridization probes will be included. For protein level prognosis kits, typically antibodies will be used to quantitate or detect the appropriate gene products. Typically instructions will be provided, which may include buffers or instructions for proper disposal of the materials.

Diagnostic, Therapeutic Applications

After prostate cancer has been identified, tests are performed to find out if cancer cells have spread within the prostate or to other parts of the body. Prostate cancer is typically classified into stages I-IV. The following tests and procedures may be used in the staging process: radionuclide bone scan, pelvic lymphadenectomy, CT scan, and seminal vesicle biopsy.

The list of targets may have other diagnostic applications besides outcome prediction. These identified markers may be valuable in such stage subsetting, distinct from outcome subsetting. Typically, after initial diagnosis, tests are performed to determine if cancer cells have spread within the prostate or to other parts of the body. Evaluation of the identified markers, singly or in combinations, may substitute for other tests to assign stage, or add to them for confirmation. Alternatively, the detection of one or more of these markers may be used as early detection screens for prostate cancer. Preferably, if the marker is soluble or released into a readily accessible body fluid, e.g., serum, semen, or urine, a diagnostic test for detection may allow for early detection of prostate cancer.

The invention is illustrated further by the following examples that are not to be construed as limiting the invention in scope to the specific procedures described in it.

EXAMPLES

Example 1. Study Design

Tissue Collection and Preparation of RNA

A cohort of 72 fresh-frozen prostate cancers was collected from patients with localized prostate cancer treated by radical prostatectomy RP at St. Vincent's Hospital, Sydney. The primary outcome, disease-specific relapse, was measured from the date of RP and was defined as a rise in serum PSA above 0.3 ng/ml with subsequent further rises. Following inking of the external limits of the prostate immediately after removal and prior to formalin-fixation, up to six, 5 mm core biopsies were taken and stored at –80 °C for a later RNA extraction. The proportion of invasive cancer in the biopsy sample was then estimated retrospectively by either frozen sectioning of the biopsy and hematoxylin and eosin staining, or by examination of archival formalin-fixed, paraffin-embedded tissue surrounding the biopsy site. Only those biopsies that

contained ≥ 75% invasive cancer were used for subsequent transcript profiling. Only one biopsy per patient was analyzed.

Xenograft model

The androgen-dependent LuCaP-35 (7) prostate cancer xenograft was grown as subcutaneous tumors in nude male mice. To study the androgen-withdrawal process, tumor-bearing mice were castrated and monitored for tumor regression and PSA levels. Tumors were harvested from mice prior to castration, and at various time points (1-100 days) post-castration and were processed for microarray analysis. For data analysis and identification of androgen-regulated genes, the samples were binned in two groups consisting of days 0-2 and days 5-100 post-castration. Genes that showed a significant ($P < 0.01$) difference in the means of each group were identified by a standard Student's t-Test.

RNA extraction and Microarray Protocols

Preparation of total RNA from fresh-frozen prostate and xenograft tissue was performed by extraction with Trizol reagent (Life Technologies Inc., Gaithersburg, MD) and was reverse transcribed using a primer containing oligo(dT) and a T7 promoter sequence. The resulting cDNAs were then *in vitro* transcribed in the presence of biotinylated nucleotides (Bio-11-CTP and Bio-16-UTP) using the T7 MEGAscript kit (Ambion, Austin, Texas).

The biotinylated targets were hybridized to the Eos Hu03, a customized Affymetrix GENECHIP® (Affymetrix, Santa Clara, California) oligonucleotide array comprising 59,619 probesets representing 46,000 unique sequences including both known and FGENESH predicted exons that were based on the first draft of the human genome. Hybridization signals were visualised using phycoerythrin-conjugated streptavidin (Molecular Probes, Eugene, Oregon). Normalization of the data was performed as follows. The probe-level intensity data from each array were fitted to a fixed gamma distribution with a mean of 300 and a shape parameter of 0.81. This normalization procedure removes between chip variation attributable to non-biological factors. Then for each probeset, a single measure of average intensity was calculated using Tukey's trimean of the intensity of the constituent probes (8). Finally, a correction for nonspecific hybridization was applied, in which the average intensity measure of a "null" probeset consisting of probes with scrambled sequence was subtracted from all other probesets on the chip.

Statistical Methods

Prior to survival analysis, a screen was applied to the expression data to eliminate probesets without meaningful variation. For each probeset, the ratio of the 90th percentile to the 15th percentile intensity measure was required to be at least 2, and the minimum expression level was required to be at least 150 average intensity units. Separate Cox proportional hazards analyses with pretreatment PSA concentration dichotomised at 20 ng/ml and gene expression modeled as a continuous variable were used to identify gene expression that correlated with PSA recurrence (9). The IQR hazards ratio was computed by multiplying the regression coefficient for each probeset by its own interquartile range prior to exponentiation. The positive false discovery rate (pFDR) was calculated using the method described by Storey and Tibshirani (10). Schoenfeld residuals were used to assess the proportional hazards assumption for the two probesets for *trp-p8* and the assumption was found to be upheld in both cases.

Variables of clinical relevance were also modeled in univariate analyses for their ability to predict disease-free survival in the 72 prostate cancers using the Cox proportional hazards model. *Trp-p8* mRNA expression assessed by ISH, was reported as proportions within histological groups and compared between groups using a Fisher's Exact test.

The expression dataset of 277 selected probesets from 72 samples was reordered according to cluster analysis in both dimensions (probesets and samples). In each analysis, the distance metric was the square root of (1-r), where r is the standard pearson product-moment correlation. The clustering algorithm used was Ward's minimum variance method (11).

In order to evaluate the ability of the 11 genes used by Singh *et al.*, to accurately predict relapse status in aggregate in our dataset, we entered these eleven probesets into a multivariate Cox regression model, and used variable selection methods to choose a subset of predictors. Three different methods were used (forward selection, backward elimination, and stepwise selection), all using $P = 0.15$ as inclusion/exclusion criterion). In each case, the final model using 4 probesets had a significance level of $P = 0.0029$ by the likelihood ratio test.

All statistical analyses were performed using SAS (SAS Institute Inc., Cary, North Carolina).

Tissue Microarray and *in situ* hybridization

Tissue microarrays were constructed as described previously (12), and were comprised of prostate cancer samples from 95 patients that are part of a previously published cohort of patients treated for localized prostate cancer by RP alone at St. Vincent's Hospital, Sydney (13). In addition, 13 prostate cancer specimens were collected from patients treated for localized prostate cancer by RP who had received at least 3 months (range 3 – 10 months) of preoperative neoadjuvant hormonal treatment (5 with anti-androgens alone, 6 with a combination of a Gn-RH analogue and anti-androgens and 2 with a Gn-RH analogue alone). *Trp-p8* expression in these 13 samples was assessed on conventional tissue sections.

For ISH, a 424-base pair probe for *trp-p8* was derived from the 3' end of the *trp-p8* gene and transcribed to produce a DIG-labeled riboprobe using an RNA DIG-labeling kit (Roche, Mannheim, Germany). ISH was performed on the VENTANA DISCOVERY™ instrument (Ventana Medical Systems, Tucson, Arizona) using the RIBOMAP™ kit with protease P2 for 2 minutes (Ventana Medical Systems, Tucson, Arizona) and hybridization for 8 hours at 65 °C. Chromogenic detection was achieved with the BLUEMAP™ detection system as described by the manufacturer (Ventana Medical Systems, Tucson, Arizona).

Example 2. Expression profiling of prostate cancers

In this study, we sought to discover novel biomarkers that might predict for PSA relapse following radical prostatectomy utilizing outcome-based statistical tools to analyze gene expression profiles of 72 prostate cancers. A criteria for selection was the ability to predict recurrence better than preoperative serum PSA concentration alone, since PSA is one of only a handful of markers that provide preoperative prognostic information. The 72 prostate tissues were collected at the time of radical prostatectomy (RP) from patients undergoing treatment for localized prostate cancer at St. Vincent's Hospital Campus, Sydney, Australia. At last follow-up (median=28.25 months, range 4.9 – 90.3 months), 17 of the 72 (23.6%) patients had relapsed, of which 14 demonstrated a rise in postoperative PSA levels while 3 patients were diagnosed with a rising PSA and local recurrence of disease. Consistent with published data (5, 6, 13), the significant predictors of prostate cancer relapse in this cohort on univariate analysis were Gleason score (HR = 1.88, $P = 0.027$), surgical margins (HR = 4.90, $P = 0.035$) and preoperative PSA concentration (HR = 4.43, $P = 0.006$) (Table 1). The overall relapse rate of 23.6% and median time to relapse of 14 months in this group of 72 patients was similar to that observed in a

cohort of 732 patients treated for localized prostate cancer by RP at the same institution between 1986 and 1999 (13).

Table 3. Clinicopathological characteristics of the prostate cancer cohort (n = 72) that were utilized in the survival analysis.

Variable	HR (confidence levels)	*P*
Gleason score[a]	1.88 (1.08-3.29)	0.027
Preoperative PSA concentration <20 ng/ml *vs.* ≥ 20 ng/ml	4.43 (1.53-12.79)	0.006
Seminal vesicle involvement positive *vs.* negative	2.33 (0.88-6.14)	0.086
Surgical margins positive *vs.* negative	4.90 (1.12-21.5)	0.035

[a] Gleason score was modeled as a continuous variable.

RNA was extracted from a core biopsy taken at the time of RP for each of the 72 cases that comprised ≥ 75% cancer tissue. Biotinylated RNA from each sample was then analyzed with a customized GENECHIP® expression array, the Eos Hu03 (14). This single GENECHIP® microarray design is representative of greater than 90% of the expressed human genome based on the first public draft and comprises 59,619 probesets representative of both known and predicted genes (15). An initial screen was applied to the microarray probesets to choose genes expressed with reliable intensity and adequate cross-sample variance. This screen reduced the initial set of 59,619 probesets to a subset of 8,521 probesets for further examination.

Example 3. Survival Analysis

Each probeset's intensity value was entered as a continuous explanatory variable in a Cox proportional hazards survival analysis predicting relapse. Pretreatment PSA concentration was also entered as a predictor in each analysis. From this analysis, 264 probesets were found to be significant predictors of relapse at $P < 0.01$. To assist interpretation, we next calculated the interquartile range hazard ratio (IQR HR) for each probeset. Because the expression data are

treated here as continuous covariates, hazards ratios expressed in their natural scale illustrate only the change in risk of relapse associated with a change of 1 unit on the expression scale, a change too small to be comprehended easily. To put the hazard ratios and associated confidence limits on a more interpretable scale, we present here the hazards ratio associated with a change in expression values equivalent to 1 interquartile range (IQR) of the sample data for each probeset. The IQR is simply the 75th percentile minus the 25th percentile, and thus contains the middle 50 percent of observations.

The multiple hypothesis testing problem has been recognized as an important issue to address in microarray research. The large number of tests that are performed simultaneously on thousands of probesets greatly increases the chances of making Type I errors (or false-positive findings). To assess the effect of multiple hypothesis testing, we adapted a method developed by Storey and Tibshirani (2001) for calculating the positive false discovery rate (pFDR), an estimate of the proportion of false-positives present in a set of findings (10). This technique was developed explicitly for use with microarray data, for which the usual assumption of independence among tests is untenable. The procedure can be briefly summarized as follows. First, null data were simulated by randomly permuting the relapse status of subjects and re-performing the survival analyses. In each simulation, the number of relapsers and non-relapsers (17 and 55, respectively) remained constant, but these designations were shuffled and assigned to patients at random. The permutation was performed 500 times, and for each simulation, the number of findings at $P < 0.01$ was noted. The mean number of findings across the 500 permutations was 85.9. This figure, an estimate of the expected number of false positives under null conditions, was then divided by the number of actual findings ($n = 264$) to obtain an estimate of the proportion of false-positive findings. After the application of a correction factor (10), the final estimate for the pFDR was 23%. Thus, we can expect that approximately 61 of the 277 findings are false positives.

Identification of the candidate marker genes

The 277 probesets (Table 1A-1C) identified by survival analysis included both known genes and hypothetical genes of unknown function, as well as ESTs.

Cluster analysis performed in both dimensions on the 72 RP samples and these 277 probesets using the Ward's minimum variance procedure identified two gene expression subgroups (Fig. 1). Sixteen of the 17 patients known to have experienced a PSA relapse were

clustered in one gene expression group characterized by a relative increase in expression of 85 genes (cluster 1) and loss of expression of 179 genes (cluster 2; Fig. 1). An additional 22 patients that were disease-free at the time of censoring were located in this expression cluster, and may suggest that these patients have an increased propensity for relapse in the future. Thirty-two patients who were disease-free at the time of censoring constituted the second expression group which also included one patient who had experienced a PSA relapse.

Notably, three of the 277 probesets showing strongest correlation with relapse in our model were identified as the gene for the putative calcium channel protein, *trp-p8* (16). For all three probesets, loss of expression of *trp-p8* mRNA was associated with a significantly shorter time to PSA relapse free survival with an IQR HR of 0.26 (0.12 – 0.54; $P < 0.001$), 0.32 (0.16 – 0.66, $P = 0.0022$) and 0.27 (0.12 – 0.66, $P = 0.0045$), respectively, when PSA was included in the analysis. Notably, loss of *trp-p8* remained a significant predictor of PSA relapse when modeled alone or with Gleason score (data not shown). Subsequent analysis showed that expression of *trp-p8* mRNA was primarily restricted to the prostate. Low-level expression was detected in normal liver and no detectable expression was seen in 32 distinct other normal tissues examined by oligonucleotide microarray analysis (Fig. 2*a*). These data confirm the findings of a recent study that also showed that *trp-p8* expression was prostate-specific (16). Analysis of 23 cancer cell lines showed that *trp-p8* is only expressed at very low levels in the androgen-dependent prostate cancer cell line LnCaP, but not in the androgen independent prostate cancer cell lines, PC-3 and DU-145, consistent with previous data (16). Since this observation alone is not conclusive evidence that *trp-p8* expression is androgen-regulated, we next utilized the androgen-dependent LuCaP-35 prostate cancer xenograft model to assess changes in *trp-p8* expression that occur during transition from androgen dependence to androgen independence of prostate cancer (7). Male LuCaP-35 mice were castrated and tumors were harvested at several time points (0-100 days) after castration. High levels of *trp-p8* expression were detected on days 0-2 after castration, but not on days 5-100 post castration, and correlated significantly with PSA expression in the same mice (Pearson P = 0.080; Figure 2, B and C).

To gain further insight into the putative association of *trp-p8* with androgen regulation, we examined the levels of *trp-p8* expression in the prostate tissue of patients who were treated with androgen deprivation therapy (neoadjuvant hormonal therapy, NHT) prior to RP. *In situ* hybridization (ISH) for *trp-8* mRNA was performed on RP specimens from 13 patients who had received at least 3 months preoperative NHT and the levels compared with tissue from 95

patients treated with RP alone (Fig. 3). These latter patients formed part of a large RP cohort described previously (13). While *trp-p8* mRNA was detected in 80 of 95 (84%) prostate cancers from patients treated with RP alone, those patients who underwent NHT prior to RP demonstrated significantly less expression of *trp-p8*, with only 4 of 13 (31%) samples positive for *trp-p8* mRNA (Fisher's Exact test, $P < 0.001$; Fig. 3).

Taken together, these data from cell lines, prostate cancer xenografts and clinical specimens, combined with the original finding that *trp-p8* mRNA levels correlated strongly with prostate cancer relapse, strongly support the conclusion that *trp-p8* expression is androgen-regulated and may be associated with the transition to androgen-independent disease. A monoclonal antibody to trp-p8 can be produced that will be used to assess protein expression by immunohistochemistry in an independent cohort of formalin-fixed, paraffin-embedded prostate cancer specimens with known prostate cancer outcome (13).

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It should be apparent that given the guidance, illustrations and examples provided herein, various alternate embodiments, modifications or manipulations of the present invention would be suggested to a skilled artisan and these are included within the spirit and purview of this application and scope of the expanded claims.